

ALIGNMENT

LOCUS STMAFSAA 1203 bp DNA linear BCT 26-APR-1993
 DEFINITION S.griseus afsA gene encoding a possible A-factor biosynthesis protein.
 ACCESSION M24250
 VERSION M24250.1 GI:153148
 KEYWORDS A-factor biosynthesis.
 SOURCE Streptomyces griseus
 ORGANISM Streptomyces griseus
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptomycineae; Streptomycetaceae; Streptomyces.
 REFERENCE 1 (bases 1 to 1203)
 AUTHORS Horinouchi,S., Suzuki,H., Nishiyama,M. and Beppu,T.
 TITLE Nucleotide sequence and transcriptional analysis of the
 Streptomyces griseus gene (afsA) responsible for A-factor
 biosynthesis
 JOURNAL J. Bacteriol. 171 (2), 1206-1210 (1989)
 COMMENT Original source text: S.griseus DNA.

Alignment Scores:

Pred. No.:	7.91e-56	Length:	1203
Score:	1050.50	Matches:	201
Percent Similarity:	73.57%	Conservative:	30
Best Local Similarity:	64.01%	Mismatches:	82
Query Match:	63.86%	Indels:	1
DB:	1	Gaps:	1

US-10-017-471B-17 (1-313) x STMAFSAA (1-1203)

Qy	1 MetProGluAlaValValLeuIleAsnSerAlaSerAspAlaAsnSerIleGluGlnThr 20
	::: :::::: ::::
Db	165 ATGCCCGAAGCAGCAGTCTTGATCGATCCGGTGCCGACTATGGACGCGGAGGCCGAGGTG 224
Qy	21 AlaLeuProValProMetAlaLeuValHisArgThrArgValGlnAspAlaPheProVal 40
	:::: :: :: ::
Db	225 GTGCATCCCGTGGGGATCGAGATGGTGCACCGGACCAGGCCGGAGGACGCCTTCCGC 284
Qy	41 SerTrpIleProLysGlyGlyAspArgPheSerValThrAlaValLeuProHisAspHis 60
	:::: ::: :::
Db	285 AACTGGGTACGCCCTGGGGCGACCGGTTCGCGGTGGAAGCGGTCCCTCCGCACGACCAT 344
Qy	61 ProPhePheAlaProValHisGlyAspArgHisAspProLeuLeuIleAlaGluThrLeu 80
	::: ::
Db	345 CCCTTCTCGCTCCGGTGGGTGACGACCTGCACGATCCGCTGCTGGTCGCGGAGGCCATG 404
Qy	81 ArgGlnAlaAlaMetLeuValPheHisAlaGlyTyrGlyValProValGlyTyrHisPhe 100
	::: ::
Db	405 CGGCAGGCAGGCCATGCTCGCCTCCACGCCGGTACGGGATCCCGCTCGCTACCACTTC 464
Qy	101 LeuMetThr---LeuAspTyrThrCysHisLeuAspHisLeuGlyValSerGlyGluVal 119
	::: ::
Db	465 CTCCTGACGGAGCTGGACTACGTCTGCCATCCCGACCTCGCGTGGGGCGAGCCC 524
Qy	120 AlaGluLeuGluValGluValAlaCysSerGlnLeuLysPheArgGlyGlyGlnProVal 139
	::: :: :::
Db	525 ACCGAGATCGGCCTGGAGGTGTTCTGCTCCGACCTGAAGTGGCGGGCGGGCTCCGGCG 584

Qy	140 GlnGlyGlnValAspTrpAlaValArgArgAlaGlyArgLeuAlaAlaThrGlyThrAla	159
	:::	
Db	585 CAGGGGCGCGTCGGCTGGCGGGTGCACCGGGCGACCGGCTCGCCGCGACGGGGTGGCG	644
Qy	160 ThrThrArgPheThrSerProGlnValTyrArgArgMetArgGlyAspPheAlaThrPro	179
	::: ::: :::	
Db	645 GCGACCCGGTTAGCACGCCAAGGCCTACCGCGGATGCGCGGTGACGTCCCAGTCAG	704
Qy	180 ThrAlaSerValProGlyThrAlaProValProAlaAlaArgAlaGlyArgThrArgAsp	199
	::: :::	
Db	705 GGCATATCCCTACCGAGACCGCGCCGGTCCCGGCCTCGCCGGCGGGCGGCCCGTC	764
Qy	200 GluAspValValLeuSerAlaSerSerGlnGlnAspThrTrpArgLeuArgValAspThr	219
	::: ::::::	
Db	765 GAGGACGTGGTGCCTCGGGGACGGGGAGGTCTGGAACTGCGCGTGGACACC	824
Qy	220 SerHisProThrLeuPheGlnArgProAsnAspHisValProGlyMetLeuLeuGlu	239
Db	825 CGGCATCCGACCCCTCTCCAGCGCCCCAACGACCACGTCCGGCATGCTCCTGCTGGAG	884
Qy	240 AlaAlaArgGlnAlaAlaCysLeuValThrGlyProAlaProPheValProSerIleGly	259
Db	885 GCGGCCCGTCAGGCCGCGCTGGTGGCGGGGCCGCGGAATCGTTCCGGTGGAGGCG	944
Qy	260 GlyThrArgPheValArgTyrAlaGluPheAspSerProCysTrpIleGlnAlaThrVal	279
	:::	
Db	945 CGCACCCGGTCCACCGGTACTCCGAGTTGGCAGCCCGTGGATAGGGCGGTGGTC	1004
Qy	280 ArgProGlyProAlaAlaGlyLeuThrThrValArgValThrGlyHisGlnAspGlySer	299
	:::	
Db	1005 CAGCCGGGGCGGACGAGGATACGGTGACCGTCCGGTGACAGGCCATCAGGACGGCGAG	1064
Qy	300 LeuValPheLeuThrThrLeuSerGlyProAlaPheSerGly	313
Db	1065 ACGGTCTTCTCACGGTCTGTCCGGCCCCGGGCCACGGC	1106

LOCUS AB001608 1215 bp DNA linear BCT 22-NOV-1997
 DEFINITION Streptomyces virginiae DNA for BarX, complete cds.
 ACCESSION AB001608
 VERSION AB001608.1 GI:2641955
 KEYWORDS BarX.
 SOURCE Streptomyces virginiae
 ORGANISM Streptomyces virginiae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptomycineae; Streptomycetaceae; Streptomyces.
 REFERENCE 1 (sites)
 AUTHORS Kinoshita,H., Ipposhi,H., Okamoto,S., Nakano,H., Nihira,T. and
 Yamada,Y.
 TITLE Butyrolactone autoregulator receptor protein (BarA) as a
 transcriptional regulator in *Streptomyces virginiae*
 JOURNAL J. Bacteriol. 179 (22), 6986-6993 (1997)
 REFERENCE 2 (bases 1 to 1215)
 AUTHORS Kinoshita,H.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAR-1997) Hiroshi Kinoshita, Osaka University,
 Department of Engineering; Yamadaoka 2-1, Suita, Osaka 565, Japan
 (E-mail:kinosita@biochem.bio.eng.osaka-u.ac.jp, Tel:+81-6-879-7433,
 Fax:+81-6-879-7432)

Alignment Scores:

Pred. No.:	5.99e-26	Length:	1215
Score:	562.50	Matches:	126
Percent Similarity:	56.12%	Conservative:	39
Best Local Similarity:	42.86%	Mismatches:	118
Query Match:	34.19%	Indels:	11
DB:	1	Gaps:	3

US-10-017-471B-17 (1-313) x AB001608 (1-1215)

Qy	19 GlnThrAlaLeuPro-----ValProMetAlaLeuVal 29
Db	214 CAGACCGGCCGACCGGCCGCGCATGGCCATGACCAGCACGGTCCGGAGCTGGTC 273
Qy	30 HisArgThrArgValGlnAspAlaPheProValSerTrpIleProLysGlyGlyAspArg 49
	:::: ::::
Db	274 CACCGGGCGGGCGGTGCGCGAACGTTCTGACGGGATGGAGGCCGACCGCGGAGAACCGA 333
Qy	50 PheSerValThrAlaValLeuProHisAspHisProPhePheAlaProValHisGlyAsp 69
	::: :: :::
Db	334 TTCCGCCCTGACGGCGCAGTGGCCCAGGGCGCACAGCTACTTCACCCCGGTGAACGGC--- 390
Qy	70 ArgHisAspProLeuLeuIleAlaGluThrLeuArgGlnAlaAlaMetLeuValPheHis 89
	:::: :: : :::
Db	391 TGCTACGACCCGCTGCTGGCCTCCGAAACCATCCGACAGGTCGGTACCCCTCTCCCCAC 450
Qy	90 AlaGlyTyrGlyValProValGlyTyrHisPheLeuMet---ThrLeuAspTyrThrCys 108
	:: :::::
Db	451 GCGGAGTTGGGGTCTCGTTCGGGGACCAAGTCCTGATGTGGGACCTCACCACAGCGTC 510
Qy	109 HisLeuAspHisLeuGlyValSerGlyGluValAlaGluLeuGluValAlaCys 128
	:::: : : :::::
Db	511 AGGCCCGAGCAGGCGGGCGTCGGTGCGCCCCGGCGACCTGGAACTGGACGTCATCTGT 570

Qy	129	SerGlnLeuLysPheArgGlyGlyGlnProValGlnGlyGlnValAspTrpAlaValArg	148
		:::::::::: :::: :::: :::: ::::	
Db	571	TCCGACATCCGCCGCCGCCGGCCGCCCTGGCGGGCATGCGCTACGAGGTACCCCTAC	630
Qy	149	ArgAlaGlyArgLeuAlaAlaThrGlyThrAlaThrThrArgPheThrSerProGlnVal	168
	:		
Db	631	TGCGGCGGCCAGGTGATGCCACCGGCGGCCCTCGACTGCACCAGCCCCGCCGTC	690
Qy	169	TyrArgArgMetArgGlyAspPheAlaThrProThrAlaSerValProGlyThrAlaPro	188
	: : : :		
Db	691	TACCAGCGGCTGCGCGGTGACCGGGTCGGTGCCACGGCGTGCGGCCCTGCCGAGCCG	750
Qy	189	ValProAlaAlaArgAlaGlyArgThrArgAspGluAspValValLeuSerAlaSerSer	208
	:::		
Db	751	CTCGCCCCCGCGTCGGTGGCCGCTTCCTCACCAACGGACGTCGTCCTGTCCGCCACCGAG	810
Qy	209	GlnGlnAspThrTrpArgLeuArgValAspThrSerHisProThrLeuPheGlnArgPro	228
	::: : : : :		
Db	811	CGTCCGCTGGAGTGGCAGCTGCGGGTGAGCAACAGCATCCCGTGCTTTCGACCACCT	870
Qy	229	AsnAspHisValProGlyMetLeuLeuLeuGluAlaAlaArgGlnAlaAlaCysLeuVal	248
	:: : : : : : : : : : :	:: : : : : : : : : : : : :	
Db	871	GTCGACCACGTTCCCGGCATGGTGCTGATGGAGTCCGCCGCCAGGCCAGGCCATC	930
Qy	249	ThrGlyProAlaProPheValProSerIleGlyGlyThrArgPheValArgTyrAlaGlu	268
	:: : : : : : : : : : : : : : :	: : : : : : : : : : : : : : : :	
Db	931	GACCCGTCCCGGCCGTTCTGCCGACCACGATGCCCTCCGAGTCAGCCGGTACGCCAG	990
Qy	269	PheAspSerProCysTrpIleGlnAlaThrValArgProGlyProAlaAlaGlyLeuThr	288
Db	991	CTCGACAGGCCCTGCTGGATACAGGCGAGGCCGCTGCCGCCAGGCCACACGGCAGCCGG	1050
Qy	289	ThrValArgValThrGlyHisGlnAspGlySerLeuValPhe	302
		: : : : : : : : : : : : : : : :	
Db	1051	CAGGTCCCGCTCACCGGCCACCAAGGACGACACCACCGTCTTC	1092